Title	Research in evolution and ecology of marine planktonic communities
Author(s)	Hernandez-Velazquez, Rodrigo
Citation	京都大学化学研究所スーパーコンピュータシステム研究成果報告書 (2018), 2017: 14-14
Issue Date	2018-03
URL	http://hdl.handle.net/2433/230717
Right	
Type	Article
Textversion	publisher

海洋性プランクトン群の進化と生態についての研究

Research in evolution and ecology of marine planktonic communities

Chemical Life Science Laboratory, Institute for Chemical Research, Kyoto University
Hernandez-Velazquez Rodrigo

研究成果概要

In regard to my project:

- I try to decipher which NCLDVs viruses (also named Megavirales) present in the epipelagic oceans infect eukaryotic hosts, conducting co-occurence association analyses. For such task I am using a matrix containing the abundance information of both 18S rRNA genes and polymerase B marker genes, the former corresponding to eukaryotes and the later to viruses. Since typical correlation analyses are prone to strong biases caused by compositional effects, approaches considering the nature of the data are being used.

To conduct this research project I make use of the SuperComputer System of Institute for Chemical Research, Kyoto University. I am using the software SparCC[1] that considers compositional effects on datasets, and very recently I have started using fastspar which is the c++ implementation of SparCC[1]. In the coming days for the same purpose I will start using CoNet[2] which combines several correlation methods and weighting strategies.

References

1 Friedman J, Alm EJ: Inferring correlation networks from genomic survey data.
PLoS Comput Biol. 2012; 8(9): e1002687

2 Faust K and Raes J. CoNet app: inference of biological association networks using Cytoscape [version 2; referees: 2 approved] F1000Research 2016, 5:1519 (doi: 10.12688/f1000research.9050.2)